

1 CCCTTTAAAG AGGGCTTTTA TATATTAATC ACAAATCACT TATGACAAAT
51 CACAAGTGAT TTGTGATTGT TGATGATAAA ATAAGAATAA GAAGAAATAG
101 AAAGAAGTGA GTGATTGTGG GAAATTTAGG CGCACAAAAA GAAAGAGTGT
-35
151 GACAAAACAT GGTTATGCTA CATGTTTAAG GTAAAAATAG TTATGTCACA
-10
201 ACTACTTATT TTTTACCCA ATCTTCTAGA CTATAATTAA AATTAAATAA
XbaI
M T I P D A N A I Y
251 CTCAATTCCG AGGTACTAAC ATGACTATAC CTGACGCAA TGCAATCTAT
RBS START
H N S A I K E V V F I K N V I K S
301 CATAACTCAG CCATCAAAGA GGTGTCTTT ATCAAGAACG TGATCAAAAG
DdeI DpnI
P N I E I G D Y T Y Y D D P V N
351 TCCCAATATT GAAATTGGGG ACTACACCTA TTATGATGAC CCAGTAAATC
SspI
P T D F E K H V T H H Y E F L G D
401 CCACCGATTT TGAGAAACAC GTTACCCATC ACTATGAATT TCTAGGCGAC
K L I I G K F C S L A S G I E F I
451 AAATTAATCA TCGGTAAATT TTGTTCTCTC GCCAGTGGCA TTGAATTTAT
M N G A N H V M K G I S T Y P F
501 CATGAACGGT GCCAACCACG TAATGAAAGG TATTTCGACT TATCCATTTA
TaqI
N I L G G D W Q Q Y T P E L T D L
551 ATATATTAGG TGGCGATTGG CAACAATACA CTCCTGAACT GACTGATTTG
P L K G T V V G N D V W F G Q N V
601 CCGTTGAAAG GTGATACTGT AGTCGGAAAT GACGTGTGGT TTGGGCAAAA
T V L P G V K I G D G A I I G A
651 TGTGACCGTC CTACCAGGCG TAAAAATAGG TGACGGTGCC ATTATCGGAG
N S V V T K D V A P Y T I V G G N
701 CAAATAGTGT TGTAACAAAA GACGTCGCTC CATATACAAT TGTCGGTGGC
P I Q L I G P R F E P E V I Q A L
751 AATCCAATTC AACTCATCGG ACCAAGATTT GAACCGGAAG TTATTCGAAGC
XmnI
E N L A W W N K D I E W I T A N
801 ATTAGAAAAT CTGGCATGGT GGAATAAAGA TATTGAATGG ATAAGTCTA
N V P K L M Q T T P T L E L I N S
851 ATGTTCTTAA ACTAATGCAA ACAACACCCA CACTTGAATT GATAAACAGT
L M E K *
STOP
901 TTAATGGAAA AATAAAAAACA AAAAAGCCGT GCAAGCAATC CAAAAATGAT
951 TGTTTACACG GCCTTTACTA TTAGTGAAT CCAATTTATT AATAATAGAT
HaeIII
1001 ATGATATAACC AGTAAAAAAT AACTAGCCA CCTCTGGCGG TACTCTACTC
1051 GTATATTTTA TTTACGACCT TCTGATGATA

FIGURE 1

LNLNNDHGPDPENILPIKGNRLQFIKPTITN-ENILVGEYSYDSKRG-ESFEDQVLTH
 MKWQOQGPNEEIIPIEGNKHVQFIKPSITK-PNILVGEYSYDSKDG-ESFESQVLTH
 -----MGNPMPKMYPIEGNKSVOFIKPILEKLENVEGEYSYDSKNG-ETFDKQILYH
 -----MKYGPDPNSIYPHEEIKSVCFIKNTITN-PNIIVGDTYYSVDNGAEKFEHVTHH
 -----MTIPDANAIIYHNSAIKEVFIKNVIKS-PNIEIGDTYYDDPVNPTDFEKHVTHH
 * * * * *

YEVIGDKLIGRFGCSIGPGTTFIMNGANHMDG-STYPFHLMRGWEKYMPSLKDLPLKG
YELIGDKLILGFKFCSIGPGTTFIMNGANHMDG-STEPFNLFNGWEKHPTLEDLPYKG
YPLINDKLIGKFKCSIGPGVTIIMNGANHMDG-STYPFNLFNGWEKHPKLDQPIKG
YEFRGDKLVIKFKCAIAEGIEFIMNGANHMRNSITTYPFNIMGNGWEKATPSLEDLPFKG
YEFLGDKLIGKFKCSLASGIEFIMNGANHVMKGISTYPFNILGGDWQYTPELTDLPLKG
* * * * * : * * * * * : * * * * * : * * * * * : * * * * *

[illegible]

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IEEWLALQWNLDMKIIENENLPFIING--DIEMLKRRKRLLDDT  
IALALKVRWDLEIETINENIDCILNG--DIKVKRS-----  
INOLLDIKWNNPIDIENENIDKILDN--SIIREVIWK-----  
IDYLLQIKWWDSAQKIFSNLETCCS--DLEKIKSRD-----  
IQALENLAWNNKDIEWITANVPKLMQTPTLELINSLMEK----
```

FIGURE 2

1080 bp : restriction map

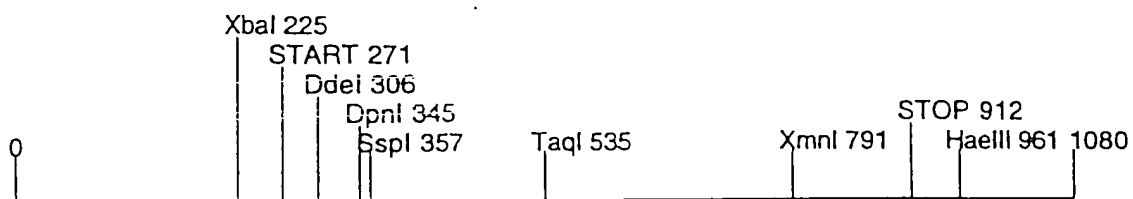


FIGURE3